

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:58:49 ; Search time 29 Seconds
(without alignments)
106.576 Million cell updates/sec

Title: US-09-300-612-1

Perfect score: 84

Sequence: 1 LKAMDPTPLWIKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	17	6 Q9TR78	Q9tr78 didelphis m
2	46	54.8	729	5 Q9VQP3	Q9vqp3 drosophila
3	46	54.8	856	5 Q9GZ10	Q9gz10 drosophila
4	46	54.8	1219	5 Q9VT64	Q9vt64 drosophila
5	46	54.8	1221	5 Q8SZR7	Q8szr7 drosophila
6	45	53.6	97	12 Q91P83	Q91p83 tomato leaf
7	45	53.6	97	12 Q91ME9	Q91me9 pepper leaf
8	45	53.6	312	6 Q9N126	Q9n126 bos taurus
9	44	52.4	125	4 Q9NV61	Q9nv61 homo sapien
10	44	52.4	377	16 Q9T32	Q9t32 rhizobium m
11	44	52.4	695	17 Q9UZG1	Q9uzg1 pyrococcus
12	44	52.4	1327	4 O15070	O15070 homo sapien
13	43	51.2	278	10 Q946H8	Q946h8 oryza sativ
14	43	51.2	354	2 Q8VM74	Q8vm74 rhizobium s
15	43	51.2	406	10 Q944S7	Q944s7 arabidopsis
16	43	51.2	687	10 Q9LMT8	Q9lmt8 arabidopsis

Q920b3 tobacco lea
O59492 pyrococcus
Q9rc28 bacillus sp
O22618 lotus corni
Q9uj46 homo sapien
Q94jh4 oryza sativ
Q9bw82 homo sapien
Q9uj45 homo sapien
Q9uj47 homo sapien
Q91x64 mus musculu
Q9nj55 anopheles g
Q9nat0 anopheles g
Q9k437 streptomyce
Q9w3h5 drosophila
Q9nwd3 homo sapien
Q9hb78 homo sapien
Q8sq02 oryza sativ
Q8vq46 escherichia
O55087 mus musculu
Q8yte5 anabaena sp
Q9cs17 mus musculu
Q9r9s3 aeromonas p
Q9cd82 mycobacteri
Q8vdm3 mus musculu
Q8xf26 salmonella
Q54123 staphylococ
O30354 salmonella
Q8wx7 homo sapien
O49889 lycopersico

17 42 50.0 97 12 Q920B3
18 42 50.0 115 17 O59492
19 42 50.0 240 2 Q9RC28
20 42 50.0 457 10 O22618
21 42 50.0 580 4 Q9UJ46
22 42 50.0 621 10 Q94JH4
23 42 50.0 809 4 Q9BW82
24 42 50.0 840 4 Q9UJ45
25 42 50.0 853 4 Q9UJ47
26 42 50.0 923 11 Q91X64
27 42 50.0 1322 5 Q9NJS5
28 42 50.0 1322 5 Q9NAT0
29 41.5 49.4 693 16 Q9K437
30 41 48.8 165 5 Q9W3H5
31 41 48.8 194 4 Q9NWD3
32 41 48.8 222 4 Q9HB78
33 41 48.8 222 10 Q8SQ02
34 41 48.8 290 2 Q8VQ46
35 41 48.8 349 11 O55087
36 41 48.8 411 16 Q8YTE5
37 41 48.8 498 11 Q9CSL7
38 41 48.8 505 2 Q9R9S3
39 41 48.8 707 16 Q9CD82
40 41 48.8 792 11 Q8VDM3
41 41 48.8 961 16 Q8XF26
42 41 48.8 967 2 Q54123
43 41 48.8 975 2 O30354
44 41 48.8 1259 4 Q8WX7
45 41 48.8 1559 10 O49889

ALIGNMENTS

RESULT 1

Q9TR78 ID Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-BOTHRIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694;
RA Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
from the serum of South American Didelphidae.";
RL Toxicon 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 100.0%; Score 84; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15

Db 1 LKAMDPTPLWIKTE 15

RESULT 2

Q9VQP3 ID Q9VQP3 PRELIMINARY; PRT; 729 AA.
AC Q9VQP3
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CG3327 protein.
GN E23 OR CG3327.

OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Chervy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Minkov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaes R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AE003580; AAF51122.1;
 DR FlyBase: FBgn002045; E23.
 DR InterPro: IPR003593; AAA_ATPase.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE= 729 AA; 82879 MW; E5D925787009069C CRC64;
 Query Match 54.8%; Score 46; DB 5; Length 729;
 Best Local Similarity 57.1%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLWIKT 14
 DB 689 LKAQNSTSPWLNT 702
 RESULT 3
 Q9GZ10
 ID Q9GZ10
 AC Q9GZ10
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21; Last annotation update)
 DE E23.
 GN E23 OR CG3327.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20402567; PubMed=10931948;
 RA Hock T., Cottrill T., Keegan J., Garza D.;
 RT "The E23 early gene of Drosophila encodes an edysone-inducible ATP-
 RT binding cassette transporter capable of repressing edysone-mediated
 RL gene activation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9519-9524(2000).
 DR EMBL: AF270979; AAG02041.1;
 DR FlyBase: FBgn002045; E23.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW ATP-binding.
 SQ SEQUENCE= 856 AA; 95080 MW; BAAE8964A5D806D6 CRC64;
 Query Match 54.8%; Score 46; DB 5; Length 856;
 Best Local Similarity 57.1%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLWIKT 14
 DB 816 LKAQNSTSPWLNT 829
 RESULT 4
 Q9VT64
 ID Q9VT64 PRELIMINARY; PRT; 1219 AA.
 AC Q9VT64
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE TAF150 protein.
 GN TAF150 OR CG6711.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Chervy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003550; AAF50190.1;
 DR FlyBase: FBgn0011836; tafi50.
 DR InterPro: IPR001930; Ala_peptase.
 DR InterPro: IPR002052; N6_Mtase.
 DR Pfam: PF01433; Peptidase_M1; 1.
 DR PROSITE: PS00092; N6_MTASE; UNKNOWN.1.
 SQ SEQUENCE 1219 AA; 139210 MW; 964683361C47D105 CRC64;

Query Match 54.8%; Score 46; DB 5; Length 1219;
 Best Local Similarity 53.3%; Pred. No. 66;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
 ||||:||||:
 Db 618 LSAMDSPVLWRLD 632

RESULT 5

ID Q8SZR7 PRELIMINARY; PRT; 1221 AA.
 AC Q8SZR7;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DE LD43729p.
 DE "Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases."
 GN TAF150.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY070564; AAL48035.1;
 SQ SEQUENCE 1221 AA; 139498 MW; C2DC066826B1AF6E CRC64;

Query Match 54.8%; Score 46; DB 5; Length 1221;
 Best Local Similarity 53.3%; Pred. No. 67;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
 ||||:||||:
 Db 620 LSAMDSPVLWRLD 634

RESULT 6

ID Q91P83 PRELIMINARY; PRT; 97 AA.
 AC Q91P83;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Vietnam tomato leaf curl geminivirus DNA A, complete
 DE sequence.
 GN C4.
 OS tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=28350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsai W.S., Hong L.T.A., Green S.K.;
 RT "Completed sequence of Vietnam tomato leaf curl geminivirus.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF264063; AAK58531.1;
 DR InterPro: IPR002488; Geminl_C4.
 DR Pfam: PF01492; Geminl_C4; 1.
 SQ SEQUENCE 97 AA; 11153 MW; D8761816CD5F94AD CRC64;

Query Match 53.6%; Score 45; DB 12; Length 97;
 Best Local Similarity 53.3%; Pred. No. 7;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
 ||||:||||:
 Db 42 LKAQMSKPIWTKTE 56

RESULT 7

ID Q91ME9 PRELIMINARY; PRT; 97 AA.
 AC Q91ME9;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE C4 protein.
 GN C4.
 OS pepper leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=83839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shih S.L., Green S.K., Ahmad I., Smith J.;
 RT "Direct submission.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF336806; AAK69638.1;
 DR InterPro: IPR002488; Geminl_C4.
 DR Pfam: PF01492; Geminl_C4; 1.
 SQ SEQUENCE 97 AA; 10965 MW; FCB6775D884266CA CRC64;

Query Match 53.6%; Score 45; DB 12; Length 97;
 Best Local Similarity 53.3%; Pred. No. 7;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
 ||||:||||:
 Db 42 LKALQMSKPMWRKTE 56

RESULT 8

ID Q9N126 PRELIMINARY; PRT; 312 AA.
 AC Q9N126;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Photoreceptor outer segment all-trans retinol dehydrogenase.
 GN PRRDH.
 OS Bos taurus (Bovine).

DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 GN Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219146; PubMed=10753906;
 RA Ratner A., Smallwood P.M., Nathans J.;
 RT "Identification and characterization of all-trans-retinol
 dehydrogenase from photoreceptor outer segments, the visual cycle
 enzyme that reduces all-trans-retinal to all-trans-retinol.";
 RL J. Biol. Chem. 275:11034-11043(2000).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AF229846; AAF63161.1; -.
 DR HSSP: P14061; 1FDS.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase; Receptor.
 SQ SEQUENCE 312 AA; 33956 MW; 36481039FF71874D CRC64;
 Query Match 53.6%; Score 45; DB 6; Length 312;
 Best Local Similarity 57.1%; Pred. NO. 24;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLWIKT 14
 DB 268 LKAMDPSGLVVRT 281
 RESULT 9
 Q9NV61 PRELIMINARY; PRT; 125 AA.
 AC Q9NV61
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE OVARC1000060 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARIAN CARCINOMA;
 RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 RA Masuho Y., Kanehori K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK001769; BAA91896.1; -.
 SQ SEQUENCE 125 AA; 13504 MW; F2D324918E3A70B1 CRC64;
 Query Match 52.4%; Score 44; DB 4; Length 125;
 Best Local Similarity 46.2%; Pred. NO. 13;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KAMDPTPLWIKT 14
 DB 4 KSMGAPPWRMRS 16
 RESULT 10
 Q92T32 PRELIMINARY; PRT; 377 AA.
 ID Q92T32
 AC Q92T32
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Putative permease ABC transporter protein.
 GN R00154 OR SMC02830.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OC NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Gostard T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL: AL591782; CAC41541.1; -.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 KW Complete proteome.
 SQ SEQUENCE 377 AA; 41867 MW; D8E34131C7E14415 CRC64;
 Query Match 52.4%; Score 44; DB 16; Length 377;
 Best Local Similarity 60.0%; Pred. NO. 41;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 6 PTPPLWIKTE 15
 DB 125 PTPPFWLMSE 134
 RESULT 11
 Q9UZG1 PRELIMINARY; PRT; 695 AA.
 ID Q9UZG1
 AC Q9UZG1
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Hypothetical protein PAB1590.
 GN PAB1590.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OC NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;
 RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ248286; CAB50098.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 695 AA; 79999 MW; 371E0E402210F551 CRC64;
 Query Match 52.4%; Score 44; DB 17; Length 695;
 Best Local Similarity 54.5%; Pred. NO. 78;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AMDPTPLWIK 13
 DB 561 ANDPKPPWLE 571
 RESULT 12
 Q15070 PRELIMINARY; PRT; 1327 AA.
 ID Q15070
 AC Q15070;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE KIAA0364 protein.
 GN KIAA0364.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=37349984; PubMed=9205841;
 RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.;
 RA "Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL DNA Res. 4:141-150(1997).
 DR EMBL; AB002362; BAA20819.1;
 DR HSSP; P43626; INKR.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 11.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00410; IG_like; 7.
 KW Immunoglobulin domain.
 SQ SEQUENCE 1327 AA; 147972 MW; 736C689FEC94D2E1 CRC64;

Query Match 52.4%; Score 44; DB 4; Length 1327;
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 MDPTPLWIKT 14
 |||||
 DB 25 MDPQPELWIES 35

RESULT 13

O946H8
 ID O946H8 PRELIMINARY; PRT; 278 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Alpha-expansin.
 GN EXP24.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21521099; PubMed=11641069;
 RA Lee Y., Choi D., Kende H.;
 RT "Expansins: ever-expanding numbers and functions."
 RL Curr. Opin. Plant Biol. 4:527-532(2001).
 DR EMBL; AF394559; AAL24495.1;
 DR InterPro: IPR000882; Pollen_allergen.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR ProDom; PD002179; Pollen_allergen; 1.
 SQ SEQUENCE 278 AA; 30046 MW; D78E729F091766F0 CRC64;

Query Match 51.2%; Score 43; DB 10; Length 278;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 DPTPLWIK 13
 |||||
 DB 44 DETPPVWLK 52

RESULT 14

O8VM74

ID O8VM74 PRELIMINARY; PRT; 354 AA.
 AC O8VM74;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative LuxA.
 OS Rhizobium sp. (strain BR816).
 OC Plasmid pSyma.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=48291;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR816;
 RA Luyten E., Verreth C., Vanderleyden J.;
 RA "Conservation of short-chain alcohol dehydrogenase in rhizobial spp."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR816;
 RA Luyten E., Swinnen E., Verreth C., Vlassak K., Dombrecht B.,
 RA Vanderleyden J.;
 RA "Functional and structural analysis of a P450 homolog gene identified
 RT in Rhizobium sp. BR816."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U26451; AAL61964.1;
 DR InterPro: IPR002103; Bac_luciferase.
 DR Pfam; PF00295; bac_luciferase; 1.
 KW Plasmid.
 SQ SEQUENCE 354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;

Query Match 51.2%; Score 43; DB 2; Length 354;
 Best Local Similarity 85.7%; Pred. No. 56;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 PTPPLWI 12
 |||||
 DB 167 PTPPIWI 173

RESULT 15

O944S7
 ID O944S7 PRELIMINARY; PRT; 406 AA.
 AC O944S7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Atlg17920/F2h15.22.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Teriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF424554; AAL11548.1;
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR002913; START.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF01852; START; 1.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.

SQ SEQUENCE 406 AA; 45986 MW; 045B92F725BD785C CRC64;
 Query Match 51.2%; Score 43; DB 10; Length 406;
 Best Local Similarity 46.7%; Pred. No. 65;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKANDPTPLWIKIE 15
 I : : | : : : : :
 Db 225 LRLQTNPLWIKTD 239

Search completed: June 27, 2003, 18:02:00
 Job time : 31 secs